

SEQUENCE LISTING

<110> Acton, Susan L. et al.

<120> ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC
DIAGNOSTIC USES THEREFOR

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<150> 09/407,427

<151> 1999-09-29

<150> 09/163,648

<151> 1998-09-30

<150> 08/989,299

<151> 1997-12-11

<160> 107

<170> PatentIn Ver. 2.0

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0963501-080900

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Val	Leu	Ser	Glu	Asp	Lys	Ser	Lys	Arg	Leu	Asn	Thr	Ile	Leu	Asn	Thr	
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Pro	Leu	Tyr	Glu	His	Leu	His	Ala	Tyr	Val	Arg	Ala	Lys	Leu	Met	Asn	
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aca Thr	gct Ala	tgg Trp	gac Asp 350	ctg Leu	ggg Gly	aag Lys	ggc Gly	gac Asp 355	ttc Phe	agg Arg	atc Ile	ctt Leu	atg Met 360	tgc Cys	aca Thr	1167
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<212> PRT

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Asn	Tyr	Asn	Thr	Asn	Ile	Thr	Glu	Glu	Asn	Val	Gln	Asn	Met	Asn	Asn
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Tyr Cys Asp Pro Ala Ser Leu Phe His Val Ser Asn Asp Tyr Ser Phe
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Ile Arg Tyr Tyr Thr Arg Thr Leu Tyr Gln Phe Gln Phe Gln Glu Ala
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Ala Asn Leu Lys Pro Arg Ile Ser Phe Asn Phe Phe Val Thr Ala Pro
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Lys Asn Val Ser Asp Ile Ile Pro Arg Thr Glu Val Glu Lys Ala Ile
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Arg Met Ser Arg Ser Arg Ile Asn Asp Ala Phe Arg Leu Asn Asp Asn
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Pro Pro Val Ser Ile Trp Leu Ile Val Phe Gly Val Val Met Gly Val
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Ile Val Val Gly Ile Val Ile Leu Ile Phe Thr Gly Ile Arg Asp Arg
755 760 765

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<213> Homo sapiens

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 <212> PRT
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 35 40 45
 Ser Gln Thr Thr Thr His Gln Ala Thr Ala His Gln Thr Ser Ala Gln
 50 55 60
 Ser Pro Asn Leu Val Thr Asp Glu Ala Glu Ala Ser Lys Phe Val Glu
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006080-0350

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 <213> Murine sp.

<220>
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			20					25					30					
Asp	His	Val	Thr	Ala	Asn	Gln	Gly	Ile	Thr	Asn	Gln	Ala	Thr	Thr	Arg			
		35					40					45						
Ser	Gln	Thr	Thr	Thr	His	Gln	Ala	Thr	Ile	Asp	Gln	Thr	Thr	Gln	Ile			
	50					55					60							
Pro	Asn	Leu	Glu	Thr	Asp	Glu	Ala	Lys	Ala	Asp	Arg	Phe	Val	Glu	Glu			
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Tyr	Asp	Arg	Thr	Ala	Gln	Val	Leu	Leu	Asn	Glu	Tyr	Ala	Glu	Ala	Asn			
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Trp	Gln	Tyr	Asn	Thr	Asn	Ile	Thr	Ile	Glu	Gly	Ser	Lys	Ile	Leu	Leu			
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Glu	Lys	Ser	Thr	Glu	Val	Ser	Asn	His	Thr	Leu	Lys	Tyr	Gly	Thr	Arg			
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Ala	Lys	Thr	Phe	Asp	Val	Ser	Asn	Phe	Gln	Asn	Ser	Ser	Ile	Lys	Arg			
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Ile	Ile	Lys	Lys	Leu	Gln	Asn	Leu	Asp	Arg	Ala	Val	Leu	Pro	Pro	Lys			
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Tyr Gly Ser Glu Tyr Ile Asn Leu Asp Gly Pro Ile Pro Ala His Leu
290 295 300

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305 310 315 320

Ala Pro Phe Pro Ser Ala Pro Asn Ile Asp Ala Thr Glu Ala Met Ile
325 330 335

Lys Gln Gly Trp Thr Pro Arg Arg Ile Phe Lys Glu Ala Asp Asn Phe
340 345 350

Phe Thr Ser Leu Gly Leu Leu Pro Val Pro Pro Glu Phe Trp Asn Lys
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Ser Met Leu Glu Lys Pro Thr Asp Gly Arg Glu Val Val Cys His Pro
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Ser Ala Trp Asp Phe Tyr Asn Gly Lys Asp Phe Arg Ile Lys Gln Cys
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Thr Ser Val Asn Met Glu Asp Leu Val Ile Ala His His Glu Met Gly
405 410 415

His Ile Gln Tyr Phe Met Gln Tyr Lys Asp Leu Pro Val Thr Phe Arg
420 425 430

Glu Gly Ala Asn Pro Gly Phe His Glu Ala Ile Gly Asp Ile Met Ala
435 440 445

Leu Ser Val Ser Thr Pro Lys His Leu Tyr Ser Leu Asn Leu Leu Ser
450 455 460

Thr Glu Gly Ser Gly Tyr Glu Tyr Asp Ile Asn Phe Leu Met Lys Met
465 470 475 480

Ala Leu Asp Lys Ile Ala Phe Ile Pro Phe Ser Tyr Leu Ile Asp Gln
485 490 495

Trp Arg Trp Arg Val Phe Asp Gly Ser Ile Thr Lys Glu Asn Tyr Asn
500 505 510

Gln Glu Trp Trp Ser Leu Arg Leu Lys Tyr Gln Gly Leu Cys Pro Pro
515 520 525

Val Pro Arg Ser Gln Gly Asp Phe Asp Pro Gly Ser Lys Phe His Val
530 535 540

Pro Ala Asn Val Pro Tyr Val Arg Tyr Phe Val Ser Phe Ile Ile Gln
545 550 555 560

Phe Gln Phe His Glu Ala Leu Cys Arg Ala Ala Gly His Thr Gly Pro
565 570 575

Leu His Lys Cys Asp Ile Tyr Gln Ser Lys Glu Ala Gly Lys Leu Leu
580 585 590

Ala Asp Ala Met Lys Leu Gly Tyr Ser Lys Pro Trp Pro Glu Ala Met

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595 600 605

Lys Leu Ile Thr Gly Gln Pro Asn Met Ser Ala Ser Ala Met Met Asn
610 615 620

Tyr Phe Lys Pro Leu Thr Glu Trp Leu Val Thr Glu Asn Arg Arg His
625 630 635 640

Gly Glu Thr Leu Gly Trp Pro Glu Tyr Asn Trp Ala Pro Asn Thr Ala
645 650 655

Arg Ala Glu Gly Ser Thr Ala Glu Ser Asn Arg Val Asn Phe Leu Gly
660 665 670

Leu Tyr Leu Glu Pro Gln Gln Ala Arg Val Gly Gln Trp Val Leu Leu
675 680 685

Phe Leu Gly Val Ala Leu Leu Val Ala Thr Val Gly Leu Ala His Arg
690 695 700

Leu Tyr Asn Ile Arg Asn His His Ser Leu Arg Arg Pro His Arg Gly
705 710 715 720

Pro Gln Phe Gly Ser Glu Val Glu Leu Arg His Ser
725 730

<210> 6
<211> 737
<212> PRT
<213> *Cryptolagus cuniculus*

<220>
<223> Description of Artificial Sequence: motifs

<400> 6
Met Gly Gln Gly Trp Ala Ala Pro Gly Leu Pro Ser Leu Leu Leu Leu
1 5 10 15

Leu Leu Cys Cys Gly His Ser Leu Leu Val Pro Ser Arg Val Ala Ala
20 25 30

Arg Arg Val Thr Val Asn Gln Gly Thr Thr Ser Gln Ala Thr Thr Thr
35 40 45

Ser Lys Ala Thr Thr Ser Ile Arg Ala Thr Thr His Gln Thr Thr Ala
50 55 60

His Gln Thr Thr Gln Ser Pro Asn Leu Val Thr Asp Glu Ala Glu Ala
65 70 75 80

Ser Arg Phe Val Glu Glu Tyr Asp Arg Ser Phe Gln Ala Val Trp Asn
85 90 95

Glu Tyr Ala Glu Ala Asn Trp Asn Tyr Asn Thr Asn Ile Thr Thr Glu
100 105 110

Ala Ser Lys Ile Leu Leu Gln Lys Asn Met Gln Ile Ala Asn His Thr
115 120 125

005080 "0954" 0950

Leu Thr Tyr Gly Asn Trp Ala Arg Arg Phe Asp Val Ser Asn Phe Gln
130 135 140

Asn Ala Thr Ser Lys Arg Ile Ile Lys Lys Val Gln Asp Leu Gln Arg
145 150 155 160

Ala Val Leu Pro Val Lys Glu Leu Glu Glu Tyr Asn Gln Ile Leu Leu
165 170 175

Asp Met Glu Thr Ile Tyr Ser Val Ala Asn Val Cys Arg Val Asp Gly
180 185 190

Ser Cys Leu Gln Leu Glu Pro Asp Leu Thr Asn Leu Met Ala Thr Ser
195 200 205

Arg Lys Tyr Asp Glu Leu Leu Trp Val Trp Thr Ser Trp Arg Asp Lys
210 215 220

Val Gly Arg Ala Ile Leu Pro Tyr Phe Pro Lys Tyr Val Glu Phe Thr
225 230 235 240

Asn Lys Ala Ala Arg Leu Asn Gly Tyr Val Asp Ala Gly Asp Ser Trp
245 250 255

Arg Ser Met Tyr Glu Thr Pro Thr Leu Glu Gln Asp Leu Glu Arg Leu
260 265 270

Phe Gln Glu Leu Gln Pro Leu Tyr Leu Asn Leu His Ala Tyr Val Gly
275 280 285

Arg Ala Leu His Arg His Tyr Gly Ala Gln His Ile Asn Leu Glu Gly
290 295 300

Pro Ile Pro Ala His Leu Leu Gly Asn Met Trp Ala Gln Thr Trp Ser
305 310 315 320

Asn Ile Tyr Asp Leu Val Ala Pro Phe Pro Ser Ala Ser Thr Met Asp
325 330 335

Ala Thr Glu Ala Met Ile Lys Gln Gly Trp Thr Pro Arg Arg Met Phe
340 345 350

Glu Glu Ala Asp Lys Phe Phe Ile Ser Leu Gly Leu Leu Pro Val Pro
355 360 365

Pro Glu Phe Trp Asn Lys Ser Met Leu Glu Lys Pro Thr Asp Gly Arg
370 375 380

Glu Val Val Cys His Ala Ser Ala Trp Asp Phe Tyr Asn Gly Lys Asp
385 390 395 400

Phe Arg Ile Lys Gln Cys Thr Thr Val Asn Met Glu Asp Leu Val Val
405 410 415

Val His His Glu Met Gly His Ile Gln Tyr Phe Met Gln Tyr Lys Asp
420 425 430

Leu Pro Val Ala Leu Arg Glu Gly Ala Asn Pro Gly Phe His Glu Ala
435 440 445

0903501-080900

<213> Homo sapiens

<220>

<223> Description of Artificial Sequence: motifs

<400> 7

Met	Gly	Ala	Ala	Ser	Gly	Arg	Arg	Gly	Pro	Gly	Leu	Leu	Leu	Pro	Leu	1	5	10	15
Pro	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Gln	Pro	Ala	Leu	Ala	Leu	Asp	Pro	20	25	30	
Gly	Leu	Gln	Pro	Gly	Asn	Phe	Ser	Ala	Asp	Glu	Ala	Gly	Ala	Gln	Leu	35	40	45	
Phe	Ala	Gln	Ser	Tyr	Asn	Ser	Ser	Ala	Glu	Gln	Val	Leu	Phe	Gln	Ser	50	55	60	
Val	Ala	Ala	Ser	Trp	Ala	His	Asp	Thr	Asn	Ile	Thr	Ala	Glu	Asn	Ala	65	70	75	80
Arg	Arg	Gln	Glu	Glu	Ala	Ala	Leu	Leu	Ser	Gln	Glu	Phe	Ala	Glu	Ala	85	90	95	
Trp	Gly	Gln	Lys	Ala	Lys	Glu	Leu	Tyr	Glu	Pro	Ile	Trp	Gln	Asn	Phe	100	105	110	
Thr	Asp	Pro	Gln	Leu	Arg	Arg	Ile	Ile	Gly	Ala	Val	Arg	Thr	Leu	Gly	115	120	125	
Ser	Ala	Asn	Leu	Pro	Leu	Ala	Lys	Arg	Gln	Gln	Tyr	Asn	Ala	Leu	Leu	130	135	140	
Ser	Asn	Met	Ser	Arg	Ile	Tyr	Ser	Thr	Ala	Lys	Val	Cys	Leu	Pro	Asn	145	150	155	160
Lys	Thr	Ala	Thr	Cys	Trp	Ser	Leu	Asp	Pro	Asp	Leu	Thr	Asn	Ile	Leu	165	170	175	
Ala	Ser	Ser	Arg	Ser	Tyr	Ala	Met	Leu	Leu	Phe	Ala	Trp	Glu	Gly	Trp	180	185	190	
His	Asn	Ala	Ala	Gly	Ile	Pro	Leu	Lys	Pro	Leu	Tyr	Glu	Asp	Phe	Thr	195	200	205	
Ala	Leu	Ser	Asn	Glu	Ala	Tyr	Lys	Gln	Asp	Gly	Phe	Thr	Asp	Thr	Gly	210	215	220	
Ala	Tyr	Trp	Arg	Ser	Trp	Tyr	Asn	Ser	Pro	Thr	Phe	Glu	Asp	Asp	Leu	225	230	235	240
Glu	His	Leu	Tyr	Gln	Gln	Leu	Glu	Pro	Leu	Tyr	Leu	Asn	Leu	His	Ala	245	250	255	
Phe	Val	Arg	Arg	Ala	Leu	His	Arg	Arg	Tyr	Gly	Asp	Arg	Tyr	Ile	Asn	260	265	270	
Leu	Arg	Gly	Pro	Ile	Pro	Ala	His	Leu	Leu	Gly	Asp	Met	Trp	Ala	Gln	275	280	285	

005030-106660

Ser Trp Glu Asn Ile Tyr Asp Met Val Val Pro Phe Pro Asp Lys Pro
290 295 300

Asn Leu Asp Val Thr Ser Thr Met Leu Gln Gln Gly Trp Asn Ala Thr
305 310 315 320

His Met Phe Arg Val Ala Glu Glu Phe Phe Thr Ser Leu Glu Leu Ser
325 330 335

Pro Met Pro Pro Glu Phe Trp Glu Gly Ser Met Leu Glu Lys Pro Ala
340 345 350

Asp Gly Arg Glu Val Val Cys His Ala Ser Ala Trp Asp Phe Tyr Asn
355 360 365

Arg Lys Asp Phe Arg Ile Lys Gln Cys Thr Arg Val Thr Met Asp Gln
370 375 380

Leu Ser Thr Val His His Glu Met Gly His Ile Gln Tyr Tyr Leu Gln
385 390 395 400

Tyr Lys Asp Leu Pro Val Ser Leu Arg Arg Gly Ala Asn Pro Gly Phe
405 410 415

His Glu Ala Ile Gly Asp Val Leu Ala Leu Ser Val Ser Thr Pro Glu
420 425 430

His Leu His Lys Ile Gly Leu Leu Asp Arg Val Thr Asn Asp Thr Glu
435 440 445

Ser Asp Ile Asn Tyr Leu Leu Lys Met Ala Leu Glu Lys Ile Ala Phe
450 455 460

Leu Pro Phe Gly Tyr Leu Val Asp Gln Trp Arg Trp Gly Val Phe Ser
465 470 475 480

Gly Arg Thr Pro Pro Ser Arg Tyr Asn Phe Asp Trp Trp Tyr Leu Arg
485 490 495

Thr Lys Tyr Gln Gly Ile Cys Pro Pro Val Thr Arg Asn Glu Thr His
500 505 510

Phe Asp Ala Gly Ala Lys Phe His Val Pro Asn Val Thr Pro Tyr Ile
515 520 525

Arg Tyr Phe Val Ser Phe Val Leu Gln Phe Gln Phe His Glu Ala Leu
530 535 540

Cys Lys Glu Ala Gly Tyr Glu Gly Pro Leu His Gln Cys Asp Ile Tyr
545 550 555 560

Arg Ser Thr Lys Ala Gly Ala Lys Leu Arg Lys Val Leu Gln Ala Gly
565 570 575

Ser Ser Arg Pro Trp Gln Glu Val Leu Lys Asp Met Val Gly Leu Asp
580 585 590

Ala Leu Asp Ala Gln Pro Leu Leu Lys Tyr Phe Gln Pro Val Thr Gln
595 600 605

006030-1055360

Trp Leu Gln Glu Gln Asn Gln Gln Asn Gly Glu Val Leu Gly Trp Pro
610 615 620

Glu Tyr Gln Trp His Pro Pro Leu Pro Asp Asn Tyr Pro Glu Gly Ile
625 630 635 640

Asp Leu Val Thr Asp Glu Ala Glu Ala Ser Lys Phe Val Glu Glu Tyr
645 650 655

Asp Arg Thr Ser Gln Val Val Trp Asn Glu Tyr Ala Glu Ala Asn Trp
660 665 670

Asn Tyr Asn Thr Asn Ile Thr Thr Glu Thr Ser Lys Ile Leu Leu Gln
675 680 685

Lys Asn Met Gln Ile Ala Asn His Thr Leu Lys Tyr Gly Thr Gln Ala
690 695 700

Arg Lys Phe Asp Val Asn Gln Leu Gln Asn Thr Thr Ile Lys Arg Ile
705 710 715 720

Ile Lys Lys Val Gln Asp Leu Glu Arg Ala Ala Leu Pro Ala Gln Glu
725 730 735

Leu Glu Glu Tyr Asn Lys Ile Leu Leu Asp Met Glu Thr Thr Tyr Ser
740 745 750

Val Ala Thr Val Cys His Pro Asn Gly Ser Cys Leu Gln Leu Glu Pro
755 760 765

Asp Leu Thr Asn Val Met Ala Thr Ser Arg Lys Tyr Glu Asp Leu Leu
770 775 780

Trp Ala Trp Glu Gly Trp Arg Asp Lys Ala Gly Arg Ala Ile Leu Gln
785 790 795 800

Phe Tyr Pro Lys Tyr Val Glu Leu Ile Asn Gln Ala Ala Arg Leu Asn
805 810 815

Gly Tyr Val Asp Ala Gly Asp Ser Trp Arg Ser Met Tyr Glu Thr Pro
820 825 830

Ser Leu Glu Gln Asp Leu Glu Arg Leu Phe Gln Glu Leu Gln Pro Leu
835 840 845

Tyr Leu Asn Leu His Ala Tyr Val Arg Arg Ala Leu His Arg His Tyr
850 855 860

Gly Ala Gln His Ile Asn Leu Glu Gly Pro Ile Pro Ala His Leu Leu
865 870 875 880

Gly Asn Met Trp Ala Gln Thr Trp Ser Asn Ile Tyr Asp Leu Val Val
885 890 895

Pro Phe Pro Ser Ala Pro Ser Met Asp Thr Thr Glu Ala Met Leu Lys
900 905 910

Gln Gly Trp Thr Pro Arg Arg Met Phe Lys Glu Ala Asp Asp Phe Phe
915 920 925

006080-10555960

Thr Ser Leu Gly Leu Leu Pro Val Pro Pro Glu Phe Trp Asn Lys Ser
930 935 940

Met Leu Glu Lys Pro Thr Asp Gly Arg Glu Val Val Cys His Ala Ser
945 950 955 960

Ala Trp Asp Phe Tyr Asn Gly Lys Asp Phe Arg Ile Lys Gln Cys Thr
965 970 975

Thr Val Asn Leu Glu Asp Leu Val Val Ala His His Glu Met Gly His
980 985 990

Ile Gln Tyr Phe Met Gln Tyr Lys Asp Leu Pro Val Ala Leu Arg Glu
995 1000 1005

Gly Ala Asn Pro Gly Phe His Glu Ala Ile Gly Asp Val Leu Ala Leu
1010 1015 1020

Ser Val Ser Thr Pro Lys His Leu His Ser Leu Asn Leu Leu Ser Ser
1025 1030 1035 1040

Glu Gly Gly Ser Asp Glu His Asp Ile Asn Phe Leu Met Lys Met Ala
1045 1050 1055

Leu Asp Lys Ile Ala Phe Ile Pro Phe Ser Tyr Leu Val Asp Gln Trp
1060 1065 1070

Arg Trp Arg Val Phe Asp Gly Ser Ile Thr Lys Glu Asn Tyr Asn Gln
1075 1080 1085

Glu Trp Trp Ser Leu Arg Leu Lys Tyr Gln Gly Leu Cys Pro Pro Val
1090 1095 1100

Pro Arg Thr Gln Gly Asp Phe Asp Pro Gly Ala Lys Phe His Ile Pro
1105 1110 1115 1120

Ser Ser Val Pro Tyr Ile Arg Tyr Phe Val Ser Phe Ile Ile Gln Phe
1125 1130 1135

Gln Phe His Glu Ala Leu Cys Gln Ala Ala Gly His Thr Gly Pro Leu
1140 1145 1150

His Lys Cys Asp Ile Tyr Gln Ser Lys Glu Ala Gly Gln Arg Leu Ala
1155 1160 1165

Thr Ala Met Lys Leu Gly Phe Ser Arg Pro Trp Pro Glu Ala Met Gln
1170 1175 1180

Leu Ile Thr Gly Gln Pro Asn Met Ser Ala Ser Ala Met Leu Ser Tyr
1185 1190 1195 1200

Phe Lys Pro Leu Leu Asp Trp Leu Arg Thr Glu Asn Glu Leu His Gly
1205 1210 1215

Glu Lys Leu Gly Trp Pro Gln Tyr Asn Trp Thr Pro Asn Ser Ala Arg
1220 1225 1230

Ser Glu Gly Pro Leu Pro Asp Ser Gly Arg Val Ser Phe Leu Gly Leu
1235 1240 1245

006000-1033960

Asp Leu Asp Ala Gln Gln Ala Arg Val Gly Gln Trp Leu Leu Leu Phe
1250 1255 1260

Leu Gly Ile Ala Leu Leu Val Ala Thr Leu Gly Leu Ser Gln Arg Leu
1265 1270 1275 1280

Phe Ser Ile Arg His Arg Ser Leu His Arg His Ser His Gly Pro Gln
1285 1290 1295

Phe Gly Ser Glu Val Glu Leu Arg His Ser
1300 1305

<210> 8

<211> 1312

<212> PRT

<213> Murine sp.

<220>

<223> Description of Artificial Sequence: motifs

<400> 8

Met Gly Ala Ala Ser Gly Gln Arg Gly Arg Trp Pro Leu Ser Pro Pro
1 5 10 15

Leu Leu Met Leu Ser Leu Leu Val Leu Leu Leu Gln Pro Ser Pro Ala
20 25 30

Pro Ala Leu Asp Pro Gly Leu Gln Pro Gly Asn Phe Ser Pro Asp Glu
35 40 45

Ala Gly Ala Gln Leu Phe Ala Glu Ser Tyr Asn Ser Ser Ala Glu Val
50 55 60

Val Met Phe Gln Ser Thr Val Ala Ser Trp Ala His Asp Thr Asn Ile
65 70 75 80

Thr Glu Glu Asn Ala Arg Arg Gln Glu Glu Ala Ala Leu Val Ser Gln
85 90 95

Glu Phe Ala Glu Val Trp Gly Lys Lys Ala Lys Glu Leu Tyr Glu Ser
100 105 110

Ile Trp Gln Asn Phe Thr Asp Ser Lys Leu Arg Arg Ile Ile Gly Ser
115 120 125

Ile Arg Thr Leu Gly Pro Ala Asn Leu Pro Leu Ala Gln Arg Gln Gln
130 135 140

Tyr Asn Ser Leu Leu Ser Asn Met Ser Arg Ile Tyr Ser Thr Gly Lys
145 150 155 160

Val Cys Phe Pro Asn Lys Thr Ala Thr Cys Trp Ser Leu Asp Pro Glu
165 170 175

Leu Thr Asn Ile Leu Ala Ser Ser Arg Ser Tyr Ala Lys Leu Leu Phe
180 185 190

Ala Trp Glu Gly Trp His Asp Ala Val Gly Ile Pro Leu Lys Pro Leu
195 200 205

0065501-000500

Val Thr Pro Tyr Ile Arg Tyr Phe Val Ser Phe Val Leu Gln Phe Gln
530 535 540

Phe His Gln Ala Leu Cys Lys Glu Ala Gly His Gln Gly Pro Leu His
545 550 555 560

Gln Cys Asp Ile Tyr Gln Ser Thr Gln Ala Gly Ala Lys Leu Lys Gln
565 570 575

Val Leu Gln Ala Gly Cys Ser Arg Pro Trp Gln Glu Val Leu Lys Asp
580 585 590

Leu Val Gly Ser Asp Ala Leu Asp Ala Lys Ala Leu Leu Glu Tyr Phe
595 600 605

Gln Pro Val Ser Gln Trp Leu Glu Glu Gln Asn Gln Arg Asn Gly Glu
610 615 620

Val Leu Gly Trp Pro Glu Asn Gln Trp Arg Pro Pro Leu Pro Asp Asn
625 630 635 640

Tyr Pro Glu Gly Ile Asp Leu Glu Thr Asp Glu Ala Lys Ala Asp Arg
645 650 655

Phe Val Glu Glu Tyr Asp Arg Thr Ala Gln Val Leu Leu Asn Glu Tyr
660 665 670

Ala Glu Ala Asn Trp Gln Tyr Asn Thr Asn Ile Thr Ile Glu Gly Ser
675 680 685

Lys Ile Leu Leu Glu Lys Ser Thr Glu Val Ser Asn His Thr Leu Lys
690 695 700

Tyr Gly Thr Arg Ala Lys Thr Phe Asp Val Ser Asn Phe Gln Asn Ser
705 710 715 720

Ser Ile Lys Arg Ile Ile Lys Lys Leu Gln Asn Leu Asp Arg Ala Val
725 730 735

Leu Pro Pro Lys Glu Leu Glu Glu Tyr Asn Gln Ile Leu Leu Asp Met
740 745 750

Glu Thr Thr Tyr Ser Leu Ser Asn Ile Cys Tyr Thr Asn Gly Thr Cys
755 760 765

Met Pro Leu Glu Pro Asp Leu Thr Asn Met Met Ala Thr Ser Arg Lys
770 775 780

Tyr Glu Glu Leu Leu Trp Ala Trp Lys Ser Trp Arg Asp Lys Val Gly
785 790 795 800

Arg Ala Ile Leu Pro Phe Phe Pro Lys Tyr Val Glu Phe Ser Asn Lys
805 810 815

Ile Ala Lys Leu Asn Gly Tyr Thr Asp Ala Gly Asp Ser Trp Arg Ser
820 825 830

Leu Tyr Glu Ser Asp Asn Leu Glu Gln Asp Leu Glu Lys Leu Tyr Gln
835 840 845

0060901-080900

Met Glu Thr Thr Tyr Ser Val Ala Asn Val Cys Tyr Thr Asn Gly Thr
755 760 765

Cys Leu Ser Leu Glu Pro Asp Leu Thr Asn Ile Met Ala Thr Ser Arg
770 775 780

Lys Tyr Glu Glu Leu Leu Trp Val Trp Lys Ser Trp Arg Asp Lys Val
785 790 795 800

Gly Arg Ala Ile Leu Pro Phe Phe Pro Lys Tyr Val Asp Phe Ser Asn
805 810 815

Lys Ile Ala Lys Leu Asn Gly Tyr Ser Asp Ala Gly Asp Ser Trp Arg
820 825 830

Ser Ser Tyr Glu Ser Asp Asp Leu Glu Gln Asp Leu Glu Lys Leu Tyr
835 840 845

Gln Glu Leu Gln Pro Leu Tyr Leu Asn Leu His Ala Tyr Val Arg Arg
850 855 860

Ser Leu His Arg His Tyr Gly Ser Glu Tyr Ile Asn Leu Asp Gly Pro
865 870 875 880

Ile Pro Ala His Leu Leu Gly Asn Met Trp Ala Gln Thr Trp Ser Asn
885 890 895

Ile Tyr Asp Leu Val Ala Pro Phe Pro Ser Ala Pro Ser Ile Asp Ala
900 905 910

Thr Glu Ala Met Ile Lys Gln Gly Trp Thr Pro Arg Arg Ile Phe Lys
915 920 925

Glu Ala Asp Asn Phe Phe Thr Ser Leu Gly Leu Leu Pro Val Pro Pro
930 935 940

Glu Phe Trp Asn Lys Ser Met Leu Glu Lys Pro Thr Asp Gly Arg Glu
945 950 955 960

Val Val Cys His Ala Ser Ala Trp Asp Phe Tyr Asn Gly Lys Asp Phe
965 970 975

Arg Ile Lys Gln Cys Thr Ser Val Asn Met Glu Glu Leu Val Ile Ala
980 985 990

His His Glu Met Gly His Ile Gln Tyr Phe Met Gln Tyr Lys Asp Leu
995 1000 1005

Pro Val Thr Phe Arg Glu Gly Ala Asn Pro Gly Phe His Glu Ala Ile
1010 1015 1020

Gly Asp Val Leu Ala Leu Ser Val Ser Thr Pro Lys His Leu His Ser
1025 1030 1035 1040

Leu Asn Leu Leu Ser Ser Glu Gly Ser Gly Tyr Glu His Asp Ile Asn
1045 1050 1055

Phe Leu Met Lys Met Ala Leu Asp Lys Ile Ala Phe Ile Pro Phe Ser
1060 1065 1070

005030-030900

Pro Pro Leu Leu Leu Leu Leu Leu Leu Arg Pro Pro Pro Ala Ala
20 25 30

Leu Thr Leu Asp Pro Gly Leu Leu Pro Gly Asp Phe Ala Ala Asp Glu
35 40 45

Ala Gly Ala Arg Leu Phe Ala Ser Ser Tyr Asn Ser Ser Ala Glu Gln
50 55 60

Val Leu Phe Arg Ser Thr Ala Ala Ser Trp Ala His Asp Thr Asn Ile
65 70 75 80

Thr Ala Glu Asn Ala Arg Arg Gln Glu Glu Glu Ala Leu Leu Ser Gln
85 90 95

Glu Phe Ala Glu Ala Trp Gly Lys Lys Ala Lys Glu Leu Tyr Asp Pro
100 105 110

Val Trp Gln Asn Phe Thr Asp Pro Glu Leu Arg Arg Ile Ile Gly Ala
115 120 125

Val Arg Thr Leu Gly Pro Ala Asn Leu Pro Leu Ala Lys Arg Gln Gln
130 135 140

Tyr Asn Ser Leu Leu Ser Asn Met Ser Gln Ile Tyr Ser Thr Gly Lys
145 150 155 160

Val Cys Phe Pro Asn Lys Thr Ala Ser Cys Trp Ser Leu Asp Pro Asp
165 170 175

Leu Asn Asn Ile Leu Ala Ser Ser Arg Ser Tyr Ala Met Leu Leu Phe
180 185 190

Ala Trp Glu Gly Trp His Asn Ala Val Gly Ile Pro Leu Lys Pro Leu
195 200 205

Tyr Gln Glu Phe Thr Ala Leu Ser Asn Glu Ala Tyr Arg Gln Asp Gly
210 215 220

Phe Ser Asp Thr Gly Ala Tyr Trp Arg Ser Trp Tyr Asp Ser Pro Thr
225 230 235 240

Phe Glu Glu Asp Leu Glu Arg Ile Tyr His Gln Leu Glu Pro Leu Tyr
245 250 255

Leu Asn Leu His Ala Tyr Val Arg Arg Val Leu His Arg Arg Tyr Gly
260 265 270

Asp Arg Tyr Ile Asn Leu Arg Gly Pro Ile Pro Ala His Leu Leu Gly
275 280 285

Asn Met Trp Ala Gln Ser Trp Glu Ser Ile Tyr Asp Met Val Val Pro
290 295 300

Phe Pro Asp Lys Pro Asn Leu Asp Val Thr Ser Thr Met Val Gln Lys
305 310 315 320

Gly Trp Asn Ala Thr His Met Phe Arg Val Ala Glu Glu Phe Phe Thr
325 330 335

006080-1055550

Val Glu Glu Tyr Asp Arg Ser Phe Gln Ala Val Trp Asn Glu Tyr Ala
660 665 670

Glu Ala Asn Trp Asn Tyr Asn Thr Asn Ile Thr Thr Glu Ala Ser Lys
675 680 685

Ile Leu Leu Gln Lys Asn Met Gln Ile Ala Asn His Thr Leu Thr Tyr
690 695 700

Gly Asn Trp Ala Arg Arg Phe Asp Val Ser Asn Phe Gln Asn Ala Thr
705 710 715 720

Ser Lys Arg Ile Ile Lys Lys Val Gln Asp Leu Gln Arg Ala Val Leu
725 730 735

Pro Val Lys Glu Leu Glu Glu Tyr Asn Gln Ile Leu Leu Asp Met Glu
740 745 750

Thr Ile Tyr Ser Val Ala Asn Val Cys Arg Val Asp Gly Ser Cys Leu
755 760 765

Gln Leu Glu Pro Asp Leu Thr Asn Leu Met Ala Thr Ser Arg Lys Tyr
770 775 780

Asp Glu Leu Leu Trp Val Trp Thr Ser Trp Arg Asp Lys Val Gly Arg
785 790 795 800

Ala Ile Leu Pro Tyr Phe Pro Lys Tyr Val Glu Phe Thr Asn Lys Ala
805 810 815

Ala Arg Leu Asn Gly Tyr Val Asp Ala Gly Asp Ser Trp Arg Ser Met
820 825 830

Tyr Glu Thr Pro Thr Leu Glu Gln Asp Leu Glu Arg Leu Phe Gln Glu
835 840 845

Leu Gln Pro Leu Tyr Leu Asn Leu His Ala Tyr Val Gly Arg Ala Leu
850 855 860

His Arg His Tyr Gly Ala Gln His Ile Asn Leu Glu Gly Pro Ile Pro
865 870 875 880

Ala His Leu Leu Gly Asn Met Trp Ala Gln Thr Trp Ser Asn Ile Tyr
885 890 895

Asp Leu Val Ala Pro Phe Pro Ser Ala Ser Thr Met Asp Ala Thr Glu
900 905 910

Ala Met Ile Lys Gln Gly Trp Thr Pro Arg Arg Met Phe Glu Glu Ala
915 920 925

Asp Lys Phe Phe Ile Ser Leu Gly Leu Leu Pro Val Pro Pro Glu Phe
930 935 940

Trp Asn Lys Ser Met Leu Glu Lys Pro Thr Asp Gly Arg Glu Val Val
945 950 955 960

Cys His Ala Ser Ala Trp Asp Phe Tyr Asn Gly Lys Asp Phe Arg Ile
965 970 975

0060301-000000

His Leu Leu Gly Asn Met Trp Ala Gln Gln Trp Ser Glu Ile Ala Asp
260 265 270

Ile Val Ser Pro Phe Pro Glu Lys Pro Leu Val Asp Val Ser Ala Glu
275 280 285

Met Glu Lys Gln Ala Tyr Thr Pro Leu Lys Met Phe Gln Met Gly Asp
290 295 300

Asp Phe Phe Thr Ser Met Asn Leu Thr Lys Leu Pro Gln Asp Phe Trp
305 310 315 320

Asp Lys Ser Ile Ile Glu Lys Pro Thr Asp Gly Arg Asp Leu Val Cys
325 330 335

His Ala Ser Ala Trp Asp Phe Tyr Leu Ile Asp Asp Val Arg Ile Lys
340 345 350

Gln Cys Thr Arg Val Thr Gln Asp Gln Leu Phe Thr Val His His Glu
355 360 365

Leu Gly His Ile Gln Tyr Phe Leu Gln Tyr Gln His Gln Pro Phe Val
370 375 380

Tyr Arg Thr Gly Ala Asn Pro Gly Phe His Glu Ala Val Gly Asp Val
385 390 395 400

Leu Ser Leu Ser Val Ser Thr Pro Lys His Leu Glu Lys Ile Gly Leu
405 410 415

Leu Lys Asp Tyr Val Arg Asp Asp Glu Ala Arg Ile Asn Gln Leu Phe
420 425 430

Leu Thr Ala Leu Asp Lys Ile Val Phe Leu Pro Phe Ala Phe Thr Met
435 440 445

Asp Lys Tyr Arg Trp Ser Leu Phe Arg Gly Glu Val Asp Lys Ala Asn
450 455 460

Trp Asn Cys Ala Phe Trp Lys Leu Arg Asp Glu Tyr Ser Gly Ile Glu
465 470 475 480

Pro Pro Val Val Arg Ser Glu Lys Asp Phe Asp Ala Pro Ala Lys Tyr
485 490 495

His Ile Ser Ala Asp Val Glu Tyr Leu Arg Tyr Leu Val Ser Phe Ile
500 505 510

Ile Gln Phe Gln Phe Tyr Lys Ser Ala Cys Ile Lys Ala Gly Gln Tyr
515 520 525

Asp Pro Asp Asn Val Glu Leu Pro Leu Asp Asn Cys Asp Ile Tyr Gly
530 535 540

Ser Ala Arg Ala Gly Ala Ala Phe His Asn Met Leu Ser Met Gly Ala
545 550 555 560

Ser Lys Pro Trp Pro Asp Ala Leu Glu Ala Phe Asn Gly Glu Arg Ile
565 570 575

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Met Ser Gly Lys Ala Ile Ala Glu Tyr Phe Glu Pro Leu Arg Val Trp
580 585 590

Leu Glu Ala Glu Asn Ile Lys Asn Asn Val His Ile Gly Trp Thr Thr
595 600 605

Ser Asn Lys Cys Val Ser Ser
610 615

<210> 12
<211> 907
<212> PRT
<213> Caenorhabditis elegans

<220>
<223> Description of Artificial Sequence: motifs

<400> 12
Met Lys Phe His Ile Leu Leu Leu Leu Leu Val Gly Ala Cys Leu Pro
1 5 10 15

Val Phe Thr Gln Glu Ile Lys Pro Lys Pro Glu Leu Leu Pro Ala Asp
20 25 30

Glu Ala Pro Lys Asp Pro Glu Ala Val Phe Ser Glu Gly Glu Pro Phe
35 40 45

Glu Leu Thr Asp Ala Leu Asp Thr Pro Lys Asn Gly Ser Val Pro Val
50 55 60

Pro Glu Pro Glu Pro Lys Pro Glu Pro Glu Pro Glu Pro Glu Pro Lys
65 70 75 80

Pro Glu Pro Glu Pro Ser Pro Thr Pro Glu Pro Glu Pro Ala Ile Lys
85 90 95

Phe Asp Asn Ile Glu Ser Glu Asp Tyr Gly Asp Val Ala Glu Thr Ala
100 105 110

Ala Ser Thr Gln Pro Asp Glu Leu Asn Thr Glu Val Ile Glu Gln Leu
115 120 125

Val Asp Thr Phe Leu Asn Thr Gly Ser Ile Ala Ser Asn Lys Thr Asn
130 135 140

Lys Gly Pro Val Phe Ala Asn Pro Val Ala Gln Ala Leu Val Asn Ser
145 150 155 160

Ser Asn Tyr Trp Lys Thr Asp Asn Leu Gln Ala Pro Gly Ser Ile Lys
165 170 175

Asp Glu Glu Lys Leu Arg Ser Trp Leu Ala Gly Tyr Glu Ala Glu Ala
180 185 190

Ile Lys Val Leu Arg Glu Val Ala Leu Ser Gly Trp Arg Tyr Phe Asn
195 200 205

Asp Ala Ser Pro Ser Leu Lys Leu Ala Leu Asp Glu Ala Glu Asn Val
210 215 220

2025 RELEASE UNDER E.O. 14176

Arg Val Tyr Ile His Pro Phe His Leu
1 5

<210> 22
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:motifs

<400> 22
Arg Val Tyr Ile His Pro Phe
1 5

<210> 23
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:motifs

<400> 23
Lys Ile Asn Glu Thr Glu Asn Ser Ile Asn
1 5 10

<210> 24
<211> 8
<212> PRT
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<220>
<223> Description of Artificial Sequence:motifs

<400> 24
Ile Ala Arg Arg His Pro Tyr Phe
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<210> 25
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:motifs

<400> 25
Asn Thr Asn Ile Thr Glu Glu Asn Val Gln Asn Met Asn Asn Ala Gly
1 5 10 15

Asp Lys Trp

<210> 26
<211> 21

006030-1099950

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<400> 29
Asp Ile Ser Lys Gly Glu Asn Asn Pro Gly Phe Gln Asn Thr Asp Asp
  1                   5                   10                   15
Val Gln
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<210> 35
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<220>
<223> Description of Artificial Sequence: motifs

<400> 35
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24

<210> 36
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<223> Description of Artificial Sequence: motifs

<400> 36
tgctcttgtc ttctgagagc actg

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<210> 37
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<223> Description of Artificial Sequence: motifs

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tctgttctat ctcttcaagc aatgcc

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<210> 38
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<223> Description of Artificial Sequence: motifs

<400> 38
catctatgtg ttgaaacaca catatctgc

29

<210> 39
<211> 31
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<223> Description of Artificial Sequence: motifs

<400> 39
aggatatctt tatattagca ttctcttcag c

31

<210> 40

006080-080900

<211> 25
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<220>
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taatgcagaa gaaatagccc cgtgg 25

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<210> 44
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<223> Description of Artificial Sequence: motifs

<400> 44
gcgatttcta caatgttact aaccac 26

<210> 45
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006080" T0544350

<220>

<223> Description of Artificial Sequence:motifs

<400> 55

ggcatatgct gcacaacctt ttc

23

<210> 56

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<213> Artificial Sequence

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<223> Description of Artificial Sequence:motifs

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25

<210> 57

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:motifs

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25

<210> 58

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:motifs

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26

<210> 59

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<212> DNA

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25

<210> 60

<211> 25

<212> DNA

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005030" T0559960

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<220>
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gatgaaactg cactagttat gccc
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<210> 62
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<220>
<223> Description of Artificial Sequence: motifs
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<220>
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<210> 65
<211> 24
<212> DNA
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 $\langle 220 \rangle$

Table 1. Demographic characteristics of the study population	
Age (years)	65.0 ± 10.0
Gender (male/female)	100/100
Education (years)	12.0 ± 2.0
Occupation (white/blue)	100/100
Marital status (married/divorced/widowed)	100/100/100
Health status (good/poor)	100/100
Smoking status (smoker/non-smoker)	100/100
Alcohol consumption (yes/no)	100/100
Family size (number of children)	2.0 ± 1.0
Income (USD/month)	1000.0 ± 200.0
Religion (Christian/Muslim/Jewish)	100/100/100
Place of birth (urban/rural)	100/100
Duration of residence in the study area (years)	10.0 ± 5.0
Number of visits to the study area (times/year)	1.0 ± 0.5
Number of visits to the study area (times/month)	1.0 ± 0.5
Number of visits to the study area (times/week)	1.0 ± 0.5
Number of visits to the study area (times/day)	1.0 ± 0.5
Number of visits to the study area (times/hour)	1.0 ± 0.5
Number of visits to the study area (times/minute)	1.0 ± 0.5
Number of visits to the study area (times/second)	1.0 ± 0.5
Number of visits to the study area (times/millisecond)	1.0 ± 0.5
Number of visits to the study area (times/microsecond)	1.0 ± 0.5
Number of visits to the study area (times/nanosecond)	1.0 ± 0.5
Number of visits to the study area (times/picosecond)	1.0 ± 0.5
Number of visits to the study area (times/femtosecond)	1.0 ± 0.5
Number of visits to the study area (times/attosecond)	1.0 ± 0.5
Number of visits to the study area (times/zettosecond)	1.0 ± 0.5
Number of visits to the study area (times/yottasecond)	1.0 ± 0.5
Number of visits to the study area (times/rontosecond)	1.0 ± 0.5
Number of visits to the study area (times/sextosecond)	1.0 ± 0.5
Number of visits to the study area (times/heptosecond)	1.0 ± 0.5
Number of visits to the study area (times/octosecond)	1.0 ± 0.5
Number of visits to the study area (times/nonasecond)	1.0 ± 0.5
Number of visits to the study area (times/decasecond)	1.0 ± 0.5
Number of visits to the study area (times/hundrethsecond)	1.0 ± 0.5
Number of visits to the study area (times/thousandthsecond)	1.0 ± 0.5
Number of visits to the study area (times/ten-thousandthsecond)	1.0 ± 0.5
Number of visits to the study area (times/hundred-thousandthsecond)	1.0 ± 0.5
Number of visits to the study area (times/millionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/tenth-millionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/hundred-millionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/billionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/trillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/quadrillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/quintillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/sextillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/septillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/octillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/nonillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/decaillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/hundrethbillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/thousandbillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/ten-trillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/hundred-trillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/millionbillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/billionbillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/trillionbillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/quadrillionbillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/quintillionbillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/sextillionbillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/septillionbillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/octillionbillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/nonillionbillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/decaillionbillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/hundrethtrillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/thousandtrillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/ten-quadrillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/hundred-quadrillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/millionquadrillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/billionquadrillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/trillionquadrillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/quadrillionquadrillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/quintillionquadrillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/sextillionquadrillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/septillionquadrillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/octillionquadrillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/nonillionquadrillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/decaillionquadrillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/hundrethquadrillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/thousandquadrillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/ten-quintillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/hundred-quintillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/millionquintillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/billionquintillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/trillionquintillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/quadrillionquintillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/quintillionquintillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/sextillionquintillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/septillionquintillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/octillionquintillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/nonillionquintillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/decaillionquintillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/hundrethquintillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/thousandquintillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/ten-sextillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/hundred-sextillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/millionsextillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/billionsextillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/trillionsextillionthsecond)	1.0 ± 0.5
Number of visits to the study area (times/quadrillionsextillionthsecond)	

24

24

25

24

25

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<220>
<223> Description of Artificial Sequence: motifs
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<400> 70
ggcacacagg aagaacacac aaaat

25

<210> 71
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:motifs

<400> 71
ctctgtgcca caagtgaaga tgt

23

<210> 72
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:motifs

<400> 72
ggtctataca atctaccact tactg

25

<210> 73
<211> 23
<212> DNA
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<223> Description of Artificial Sequence:motifs

<400> 73
agccaacact tggacctcct aac

23

<210> 74
<211> 23
<212> DNA
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<400> 74
gtgaagatca ggatgacaat gcc

23

<210> 75
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<212> DNA
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<220>
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006080-1035360

25

<220>
<223> Description of Artificial Sequence: motifs

24

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<220>
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24

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23

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25

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<220>
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<400> 80

[illegible]

25

25

22

27

26

[illegible]

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<211> 26
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:motifs

<400> 91
tgaattgatt attgttgagt gcacag 26

<210> 92
<211> 23
<212> DNA
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<220>
<223> Description of Artificial Sequence:motifs

<400> 92
cgtctgaatg acaacagcct aga 23

<210> 93
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:motifs

<400> 93
cgtctgaatg acgacagcct agag 24

<210> 94
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<212> DNA
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<400> 94
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<210> 95
<211> 26
<212> DNA
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<220>
<223> Description of Artificial Sequence:motifs

<400> 95
agttgaaaac aatgatatat cattgg 26

006080-1055960

<210> 101

<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: motifs

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gttctctaac tgtagagtga atggaaa

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<210> 102
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<220>
<223> Description of Artificial Sequence: motifs

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23

<210> 103
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<400> 103
gatcgattcc aaacatcact gtaggc

26

<210> 104
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<212> DNA
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<220>
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<400> 104
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<210> 105
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20

<210> 106
<211> 805

005030"1055960

<213> Homo sapiens

Met 1	Ser	Ser	Ser	Ser 5	Trp	Leu	Leu	Leu	Ser 10	Leu	Val	Ala	Val	Thr 15	Ala
Ala	Gln	Ser	Thr 20	Ile	Glu	Glu	Gln	Ala 25	Lys	Thr	Phe	Leu	Asp 30	Lys	Phe
Asn	His	Glu 35	Ala	Glu	Asp	Leu	Phe 40	Tyr	Gln	Ser	Ser	Leu 45	Ala	Ser	Trp
Asn	Tyr 50	Asn	Thr	Asn	Ile	Thr 55	Glu	Glu	Asn	Val	Gln 60	Asn	Met	Asn	Asn
Ala 65	Gly	Asp	Lys	Trp	Ser 70	Ala	Phe	Leu	Lys	Glu 75	Gln	Ser	Thr	Leu	Ala 80
Gln	Met	Tyr	Pro	Leu 85	Gln	Glu	Ile	Gln	Asn 90	Leu	Thr	Val	Lys	Leu 95	Gln
Leu	Gln	Ala	Leu 100	Gln	Gln	Asn	Gly 105	Ser	Ser	Val	Leu	Ser	Glu 110	Asp	Lys
Ser	Lys	Arg 115	Leu	Asn	Thr	Ile	Leu 120	Asn	Thr	Met	Ser	Thr 125	Ile	Tyr	Ser
Thr 130	Gly	Lys	Val	Cys	Asn	Pro 135	Asp	Asn	Pro	Gln	Glu 140	Cys	Leu	Leu	Leu
Glu 145	Pro	Gly	Leu	Asn 150	Glu	Ile	Met	Ala	Asn	Ser 155	Leu	Asp	Tyr	Asn	Glu 160
Arg	Leu	Trp	Ala	Trp 165	Glu	Ser	Trp	Arg	Ser 170	Glu	Val	Gly	Lys	Gln 175	Leu
Arg	Pro	Leu	Tyr 180	Glu	Glu	Tyr	Val 185	Val	Leu	Lys	Asn	Glu 190	Met	Ala	Arg
Ala	Asn	His 195	Tyr	Glu	Asp	Tyr	Gly 200	Asp	Tyr	Trp	Arg	Gly 205	Asp	Tyr	Glu
Val 210	Asn	Gly	Val	Asp	Gly	Tyr 215	Asp	Tyr	Ser	Arg	Gly 220	Gln	Leu	Ile	Glu
Asp 225	Val	Glu	His	Thr	Phe 230	Glu	Glu	Ile	Lys	Pro 235	Leu	Tyr	Glu	His	Leu 240
His	Ala	Tyr	Val	Arg 245	Ala	Lys	Leu	Met	Asn 250	Ala	Tyr	Pro	Ser	Tyr 255	Ile
Ser	Pro	Ile	Gly 260	Cys	Leu	Pro	Ala	His 265	Leu	Leu	Gly	Asp	Met 270	Trp	Gly
Arg	Phe	Trp	Thr	Asn	Leu	Tyr	Ser 280	Leu	Thr	Val	Pro	Phe 285	Gly	Gln	Lys
Pro	Asn 290	Ile	Asp	Val	Thr	Asp 295	Ala	Met	Val	Asp	Gln 300	Ala	Trp	Asp	Ala

Lys Ser Ala Leu Gly Asp Lys Ala Tyr Glu Trp Asn Asp Asn Glu Met
625 630 635 640

Tyr Leu Phe Arg Ser Ser Val Ala Tyr Ala Met Arg Gln Tyr Phe Leu
645 650 655

Lys Val Lys Asn Gln Met Ile Leu Phe Gly Glu Glu Asp Val Arg Val
660 665 670

Ala Asn Leu Lys Pro Arg Ile Ser Phe Asn Phe Phe Val Thr Ala Pro
675 680 685

Lys Asn Val Ser Asp Ile Ile Pro Arg Thr Glu Val Glu Lys Ala Ile
690 695 700

Arg Met Ser Arg Ser Arg Ile Asn Asp Ala Phe Arg Leu Asn Asp Asn
705 710 715 720

Ser Leu Glu Phe Leu Gly Ile Gln Pro Thr Leu Gly Pro Pro Asn Gln
725 730 735

Pro Pro Val Ser Ile Trp Leu Ile Val Phe Gly Val Val Met Gly Val
740 745 750

Ile Val Val Gly Ile Val Ile Leu Ile Phe Thr Gly Ile Arg Asp Arg
755 760 765

Lys Lys Lys Asn Lys Ala Arg Ser Gly Glu Asn Pro Tyr Ala Ser Ile
770 775 780

Asp Ile Ser Lys Gly Glu Asn Asn Pro Gly Phe Gln Asn Thr Asp Asp
785 790 795 800

Val Gln Thr Ser Phe
805

<210> 107

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: motifs

<400> 107

Glu Leu Tyr Glu Asn Lys Pro Arg Arg Pro Tyr Ile Leu
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006080-030900